

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Hu, Sylvia
- (ii) TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic Factor
- (iii) NUMBER OF SEQUENCES: 50
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: AMGEN INC.
  - (B) STREET: 1840 DeHavilland Drive
  - (C) CITY: Thousand Oaks
  - (D) STATE: California
  - (E) COUNTRY: United States of America
  - (F) ZIP: 91320
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: Patent In Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Curry, Daniel R.
  - (B) REGISTRATION NUMBER: 32,727
  - (C) REFERENCE/DOCKET NUMBER: A-357
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 805-447-8102
  - (B) TELEFAX: 805-499-8011
  - (C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 402 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 1..402

Sub  
B?

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCA	CCA	GAT	AAA	CAA	ATG	GCA	GTG	CTT	CCT	AGA	AGA	GAG	CGG	AAT	CGG	48
Ser	Pro	Asp	Lys	Gln	Met	Ala	Val	Leu	Pro	Arg	Arg	Glu	Arg	Asn	Arg	
1				5				10						15		
CAG	GCT	GCA	GCT	GCC	AAC	CCA	GAG	AAT	TCC	AGA	GGA	AAA	GGT	CGG	AGA	96
Gln	Ala	Ala	Ala	Ala	Asn	Pro	Glu	Asn	Ser	Arg	Gly	Lys	Gly	Arg	Arg	
			20				25						30			
GGC	CAG	AGG	GGC	AAA	AAC	CGG	GGT	TGT	GTC	TTA	ACT	GCA	ATA	CAT	TTA	144
Gly	Gln	Arg	Gly	Lys	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile	His	Leu	
		35					40					45				
AAT	GTC	ACT	GAC	TTG	GGT	CTG	GGC	TAT	GAA	ACC	AAG	GAG	GAA	CTG	ATT	192
Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	
	50					55					60					
TTT	AGG	TAC	TGC	AGC	GGC	TCT	TGC	GAT	GCA	GCT	GAG	ACA	ACG	TAC	GAC	240
Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys	Asp	Ala	Ala	Glu	Thr	Thr	Tyr	Asp	
65					70				75						80	
AAA	ATA	TTG	AAA	AAC	TTA	TCC	AGA	AAT	AGA	AGG	CTG	GTG	AGT	GAC	AAA	288
Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg	Asn	Arg	Arg	Leu	Val	Ser	Asp	Lys	
				85				90						95		
GTA	GGG	CAG	GCA	TGT	TGC	AGA	CCC	ATC	GCC	TTT	GAT	GAT	GAC	CTG	TCG	336
Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro	Ile	Ala	Phe	Asp	Asp	Asp	Leu	Ser	
			100					105					110			
TTT	TTA	GAT	GAT	AAC	CTG	GTT	TAC	CAT	ATT	CTA	AGA	AAG	CAT	TCC	GCT	384
Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	Ser	Ala	
		115					120					125				
AAA	AGG	TGT	GGA	TGT	ATC											402
Lys	Arg	Cys	Gly	Cys	Ile											
		130														

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser	Pro	Asp	Lys	Gln	Met	Ala	Val	Leu	Pro	Arg	Arg	Glu	Arg	Asn	Arg	
1				5				10						15		
Gln	Ala	Ala	Ala	Ala	Asn	Pro	Glu	Asn	Ser	Arg	Gly	Lys	Gly	Arg	Arg	
			20					25					30			
Gly	Gln	Arg	Gly	Lys	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile	His	Leu	
		35					40					45				

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(2) INFORMATION FOR SEQ ID NO:3:

(ii) MOLECULE TYPE: peptide

Lys Asn Arg Gly  
1

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE/DESCRIPTION: SEQ ID NO:4:

Gly Lys Asn / Arg Gly  
1 5

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Gly Lys Asn Arg Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gln Arg Gly Lys Asn Arg Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gln Arg Gly Lys Asn Arg Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Gly Gln Arg Gly Lys Asn Arg Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
1                    5                    10

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
1                    5                    10                    15

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
1                    5                    10                    15

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg  
1 5 10 15  
Gly

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn  
1 5 10 15  
Arg Gly

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys  
1 5 10 15  
Asn Arg Gly

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly  
 1 5 10 15  
 Lys Asn Arg Gly  
 20

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg  
 1 5 10 15  
 Gly Lys Asn Arg Gly  
 20

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln  
 1 5 10 15  
 Arg Gly Lys Asn Arg Gly  
 20

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:



Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly  
1 5 10 15

Gln Arg Gly Lys Asn Arg Gly  
20

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg  
1 5 10 15

Gly Gln Arg Gly Lys Asn Arg Gly  
20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg  
1 5 10 15

Arg Gly Gln Arg Gly Lys Asn Arg Gly  
20 25

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asn Arg Gln Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly  
1 5 10 15

Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
20 25

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys  
1 5 10 15

Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
20 25

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly  
1 5 10 15

Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
20 25

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg  
1 5 10 15

Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
20 25

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID/NO:29:

Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser  
1 5 10 15

Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
20 25 30

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn  
1 5 10 15

Ser Arg Gly Lys / Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
20 25 30

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro Glu  
1 5 10 15

Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly  
 20 25 30

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro  
 1 5 10 15  
 Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg  
 20 25 30  
 Gly

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn  
 1 5 10 15  
 Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn  
 20 25 30  
 Arg Gly

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala  
 1 5 10 15  
 Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys  
 20 25 30  
 Asn Arg Gly  
 35

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala  
 1 5 10 15  
 Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly  
 20 25 30  
 Lys Asn Arg Gly  
 35

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala  
 1 5 10 15  
 Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg  
 20 25 30  
 Gly Lys Asn Arg Gly  
 35

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala
1           5           10           15
Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln
          20           25           30
Arg Gly Lys Asn Arg Gly
          35

```

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln
1           5           10           15
Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly
          20           25           30
Gln Arg Gly Lys Asn Arg Gly
          35

```

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 417 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

CATATGTCTC CCGATAAACA AATGGCTGTT CTTCCACGTC GTGAACGTAA CCGTCAGGCG 60
GCCGCTGCTA ACCCGGAGAA TTCCCGTGGT AAAGGTCGTC GTGGTCAGCG TGGTAAAAAC 120
CGCGGTTGCG TTCTGACCGC TATCCACCTG AACGTTACCG ACCTGGGTCT CGGTTACGAA 180
ACCAAAGAAG AATTAATCTT CCGTTACTGC TCCGGTTCCT GCGACGCTGC TGAAACCACG 240

```

TACGACAAAA TCCTGAAAAA CCTGTCCCGT AACCGTCGTC TGGTTTCCGA CAAAGTTGGT 300  
 CAAGCTTGCT GCCGTCCGAT CGCTTTCGAC GACGACCTGT CCTTCCTGGA CGACAACCTG 360  
 GTTTACCACA TCCTGCGTAA AACTCCGCT AAGCGTTGCG GTTGCATCTA AGGATCC 417

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 417 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CATATGAGCC CGGACAAACA GATGGCAGTA CTTCCACGTC GTGAACGTAA TCGCCAGGCA 60  
 GCAGCTGCAA ACCCGGAAAA CTCCCGTGGT AAAGGTCGCC GTGGCCAGCG CGGCAAAAAC 120  
 CGTGGTTGTG TTCTGACTGC AATCCACCTG AACGTTACTG ACCTGGGTCT GGGCTACGAA 180  
 ACCAAAGAAG AACTGATCTT CCGCTACTGC AGCGGCTCTT GCGACGCAGC TGAAACCACT 240  
 TACGACAAAA TCCTGAAAAA CCTGTCCCGT AACCGCCGTC TGGTAAGCGA CAAAGTAGGT 300  
 CAGGCATGCT GCCGTCCGAT CGCATTTCGAC GATGACCTGA GCTTCCTGGA TGACAACCTG 360  
 GTTTACCACA TCCTGCGTAA AACTCCGCT AAACGCTGCG GTTGCATCTA AGGATCC 417

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATG	TCC	CCA	GAA	AAT	TCT	CGT	GGT	AAA	GGT	CGT	CGT	GGT	CAG	CGT	GGT	48
Met	Ser	Pro	Glu	Asn	Ser	Arg	Gly	Lys	Gly	Arg	Gly	Gln	Arg	Gly		
135					140				145						150	
AAT	AAC	CGC	GGT	TGC	GTT	CTG	ACC	GCT	ATC	CAC	CTG	AAC	GTT	ACC	GAC	96
Asn	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	
				155					160						165	

CTG GGT CTC GGT TAC GAA ACC AAA GAA GAA TTA ATC TTC CGT TAC TGC 144  
 Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys  
                   170                                  175                                  180

TCC GGT TCC TGC GAC GCT GCT GAA ACC ACG TAC GAC AAA ATC CTG AAA 192  
 Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys  
                   185                                  190                                  195

AAC CTG TCC CGT AAC CGT CGT CTG GTT TCC GAC AAA GTT GGT CAA GCT 240  
 Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala  
                   200                                  205                                  210

TGC TGC CGT CCG ATC GCT TTC GAC GAC GAC CTG TCC TTC CTG GAC GAC 288  
 Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp  
                   215                                  220                                  225                                  230

AAC CTG GTT TAC CAC ATC CTG CGT AAA CAC TCC GCT AAG CGT TGC GGT 336  
 Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly  
                                   235                                  240                                  245

TGC ATC TAA 345  
 Cys Ile

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly  
   1                  5                                  10                                  15

Asn Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp  
                   20                                  25                                  30

Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys  
                   35                                  40                                  45

Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys  
                   50                                  55                                  60

Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala  
                   65                                  70                                  75                                  80

Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp  
                   85                                  90                                  95

Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly  
                   100                                  105                                  110

Cys Ile



## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..312

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATG	CGT	GGT	CAA	CGT	GGT	AAA	AAC	CGC	GGT	TGC	GTT	CTG	ACT	GCA	ATC	48
Met	Arg	Gly	Gln	Arg	Gly	Lys	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile	
115					120					125					130	
CAC	CTG	AAC	GTT	ACT	GAC	CTG	GGT	CTG	GGC	TAC	GAA	ACC	AAA	GAA	GAA	96
His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly	Tyr	Glu	Thr	Lys	Glu	Glu	
				135					140					145		
CTG	ATC	TTC	CGC	TAC	TGC	AGC	GGC	TCT	TGC	GAC	GCA	GCT	GAA	ACC	ACT	144
Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys	Asp	Ala	Ala	Glu	Thr	Thr	
			150					155					160			
TAC	GAC	AAA	ATC	CTG	AAA	AAC	CTG	TCC	CGT	AAC	CGC	CGT	CTG	GTA	AGC	192
Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg	Asn	Arg	Arg	Leu	Val	Ser	
		165					170					175				
GAC	AAA	GTA	GGT	CAG	GCA	TGC	TGC	CGT	CCG	ATC	GCA	TTC	GAC	GAT	GAC	240
Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro	Ile	Ala	Phe	Asp	Asp	Asp	
	180					185					190					
CTG	AGC	TTC	CTG	GAT	GAC	AAC	CTG	GTT	TAC	CAC	ATC	CTG	CGT	AAA	CAC	288
Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	
195				200					205					210		
TCC	GCT	AAA	CGC	TGC	GGT	TGC	ATC	TAA								315
Ser	Ala	Lys	Arg	Gly	Cys	Gly	Cys	Ile								
				215												

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Arg	Gly	Gln	Arg	Gly	Lys	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile
1					5				10					15	

His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu  
                   20                                  25                                  30  
 Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr  
                   35                                  40                                  45  
 Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser  
                   50                                  55                                  60  
 Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp  
                   65                                  70                                  75                                  80  
 Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His  
                                   85                                  90                                  95  
 Ser Ala Lys Arg Cys Gly Cys Ile  
                                   100

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..309

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATG GGT CAA CGT GGT AAA AAC CGT GGT TGT GTT CTG ACT GCA ATC CAC 48  
 Met Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His  
 105                                  110                                  115                                  120  
 CTG AAC GTT ACT GAC CTG GGT CTG GGC TAC GAA ACC AAA GAA GAA CTG 96  
 Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu  
                                   125                                  130                                  135  
 ATC TTC CGC TAC TGC AGC GGC TCT TGC GAC GCA GCT GAA ACC ACT TAC 144  
 Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr  
                                   140                                  145                                  150  
 GAC AAA ATC CTG AAA AAC CTG TCC CGT AAC CGC CGT CTG GTA AGC GAC 192  
 Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp  
                                   155                                  160                                  165  
 AAA GTA GGT CAG GCA TGC TGC CGT CCG ATC GCA TTC GAC GAT GAC CTG 240  
 Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu  
                                   170                                  175                                  180  
 AGC TTC CTG GAT GAC AAC CTG GTT TAC CAC ATC CTG CGT AAA CAC TCC 288  
 Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser  
 185                                  190                                  195                                  200

GCT AAA CGC TGC GGT TGC ATC TAA  
 Ala Lys Arg Cys Gly Cys Ile  
 205

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## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His  
 1 5 10 15  
 Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu  
 20 25 30  
 Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr  
 35 40 45  
 Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp  
 50 55 60  
 Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu  
 65 70 75 80  
 Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser  
 85 90 95  
 Ala Lys Arg Cys Gly Cys Ile  
 100

## (2) INFORMATION FOR SEQ ID NO:47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn  
 1 5 10 15  
 Arg Gln Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg  
 20 25 30  
 Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His  
 35 40 45

Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu  
 50 55 60  
 Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr  
 65 70 75 80  
 Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp  
 85 90 95  
 Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu  
 100 105 110  
 Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser  
 115 120 125  
 Ala Lys Arg Cys Gly Cys Ile  
 130 135

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile  
 1 5 10 15  
 His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu  
 20 25 30  
 Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr  
 35 40 45  
 Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser  
 50 55 60  
 Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp  
 65 70 75 80  
 Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His  
 85 90 95  
 Ser Ala Lys Arg Cys Gly Cys Ile  
 100

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met	Gly	Gln	Arg	Gly	Lys	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile	His
1				5					10					15	
Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu
			20					25					30		
Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys	Asp	Ala	Ala	Glu	Thr	Thr	Tyr
		35					40					45			
Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg	Asn	Arg	Arg	Leu	Val	Ser	Asp
	50					55					60				
Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro	Ile	Ala	Phe	Asp	Asp	Asp	Leu
65					70					75					80
Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	Ser
			85						90					95	
Ala	Lys	Arg	Cys	Gly	Cys	Ile									
					100										

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Ser	Pro	Glu	Asn	Ser	Arg	Gly	Lys	Gly	Arg	Arg	Gly	Gln	Arg	Gly
1				5					10					15	
Asn	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp
			20					25					30		
Leu	Gly	Leu	Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys
		35					40					45			
Ser	Gly	Ser	Cys	Asp	Ala	Ala	Glu	Thr	Thr	Tyr	Asp	Lys	Ile	Leu	Lys
	50					55					60				
Asn	Leu	Ser	Arg	Asn	Arg	Arg	Leu	Val	Ser	Asp	Lys	Val	Gly	Gln	Ala
65					70					75					80
Cys	Cys	Arg	Pro	Ile	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp
				85					90					95	

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Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly  
100 105 110

Cys Ile

111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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B2  
(cont.)